

Sequence listing

<110> Sagami Chemical Research Center et al.

5 <120> Human Proteins Having Hydrophobic Domains And DNAs Encoding These
Proteins

<130> 661101

10 <141> 1999-06-18

<150> JP 10-180008

<151> 1998-06-26

15 <160> 40

<170> Windows 95 (Word 98)

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20 <211> 238

<212> PRT

<213> Homo sapiens

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1 5 10 15

Tyr Cys Ser Ile Leu Cys Asn Tyr Lys Ala Ile Glu Met Pro Ser His

20 25 30

Gln Thr Tyr Gly Gly Ser Trp Lys Phe Leu Thr Phe Ile Asp Leu Val

30 35 40 45

Ile Gln Ala Val Phe Phe Gly Ile Cys Val Leu Thr Asp Leu Ser Ser

50 55 60

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Leu Leu Thr Arg Gly Ser Gly Asn Gln Glu Gln Glu Arg Gln Leu Lys
 65 70 75 80
 Lys Leu Ile Ser Leu Arg Asp Trp Met Leu Ala Val Leu Ala Phe Pro
 85 90 95
 5 Val Gly Val Phe Val Val Ala Val Phe Trp Ile Ile Tyr Ala Tyr Asp
 100 105 110
 Arg Glu Met Ile Tyr Pro Lys Leu Leu Asp Asn Phe Ile Pro Gly Trp
 115 120 125
 Leu Asn His Gly Met His Thr Thr Val Leu Pro Phe Ile Leu Ile Glu
 10 130 135 140
 Met Arg Thr Ser His His Gln Tyr Pro Ser Arg Ser Ser Gly Leu Thr
 145 150 155 160
 Ala Ile Cys Thr Phe Ser Val Gly Tyr Ile Leu Trp Val Cys Trp Val
 165 170 175
 15 His His Val Thr Gly Met Trp Val Tyr Pro Phe Leu Glu His Ile Gly
 180 185 190
 Pro Gly Ala Arg Ile Ile Phe Phe Gly Ser Thr Thr Ile Leu Met Asn
 195 200 205
 Phe Leu Tyr Leu Leu Gly Glu Val Leu Asn Asn Tyr Ile Trp Asp Thr
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 Gln Lys Ser Met Glu Glu Glu Lys Glu Lys Pro Lys Leu Glu
 225 230 235

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20 25 30
 Thr Pro Glu Ala Ala Val Leu Arg Ser Ala Ala Ala Arg Leu Arg Gln
 35 40 45
 Ile His Arg Ser Phe Phe Ser Ala Tyr Leu Gly Tyr Pro Gly Asn Arg
 5 50 55 60
 Phe Glu Leu Val Ala Leu Met Ala Asp Ser Val Leu Ser Asp Ser Pro
 65 70 75 80
 Gly Pro Thr Trp Gly Arg Val Val Thr Leu Val Thr Phe Ala Gly Thr
 85 90 95
 10 Leu Leu Glu Arg Gly Pro Leu Val Thr Ala Arg Trp Lys Lys Trp Gly
 100 105 110
 Phe Gln Pro Arg Leu Lys Glu Gln Glu Gly Asp Val Ala Arg Asp Cys
 115 120 125
 Gln Arg Leu Val Ala Leu Leu Ser Ser Arg Leu Met Gly Gln His Arg
 15 130 135 140
 Ala Trp Leu Gln Ala Gln Gly Gly Trp Asp Gly Phe Cys His Phe Phe
 145 150 155 160
 Arg Thr Pro Phe Pro Leu Ala Phe Trp Arg Lys Gln Leu Val Gln Ala
 165 170 175
 20 Phe Leu Ser Cys Leu Leu Thr Thr Ala Phe Ile Tyr Leu Trp Thr Arg
 180 185 190
 Leu Leu

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 100504-4502260

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20 25 30
 Asp Tyr Ile Asn Ala Arg Ser Cys Cys Ser Lys Leu Asn Lys Trp Val
 35 40 45
 Ile Pro Glu Leu Ile Gly His Thr Ile Val Thr Val Leu Leu Leu Met
 5 50 55 60
 Ser Leu His Trp Phe Ile Phe Leu Leu Asn Leu Pro Val Ala Thr Trp
 65 70 75 80
 Asn Ile Tyr Arg Tyr Ile Met Val Pro Ser Gly Asn Met Gly Val Phe
 85 90 95
 10 Asp Pro Thr Glu Ile His Asn Arg Gly Gln Leu Lys Ser His Met Lys
 100 105 110
 Glu Ala Met Ile Lys Leu Gly Phe His Leu Leu Cys Phe Phe Met Tyr
 115 120 125
 Leu Tyr Ser Met Ile Leu Ala Leu Ile Asn Asp
 15 130 135

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 25 Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser Gly Thr
 20 25 30
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 35 40 45
 His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr Tyr Pro Lys Glu
 30 50 55 60
 Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg Leu Phe Ser Ile Cys
 65 70 75 80

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Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg Thr Lys Leu Glu Cys
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 Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala
 100 105 110
 5 Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln
 115 120 125
 Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu
 130 135 140
 10 Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser
 145 150 155 160
 Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys
 165 170 175
 Ile Val Ile Phe Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu
 180 185 190
 15 Glu Gln Glu Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser
 195 200 205
 Tyr Leu Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu Asp
 210 215 220
 Gly Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp
 20 225 230 235 240
 Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp Ile
 245 250 255
 Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro Ser Glu
 260 265 270
 25 Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu Gln Lys Leu
 275 280 285
 Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg Ser Lys Thr Glu
 290 295 300
 Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys Val Asn Leu Ala His
 30 305 310 315 320
 Ser Glu Ile

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<211> 231

<212> PRT

<213> Homo sapiens

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 Arg Leu Met Arg Val Gly Leu Ala Leu Ile Leu Val Gly His Val Asn
 10 20 25 30
 Leu Leu Leu Gly Ala Val Leu His Gly Thr Val Leu Arg His Val Ala
 35 40 45
 Asn Pro Arg Gly Ala Val Thr Pro Glu Tyr Thr Val Ala Asn Val Ile
 50 55 60
 15 Ser Val Gly Ser Gly Leu Leu Ser Val Ser Val Gly Leu Val Ala Leu
 65 70 75 80
 Leu Ala Ser Arg Asn Leu Leu Arg Pro Pro Leu His Trp Val Leu Leu
 85 90 95
 Ala Leu Ala Leu Val Asn Leu Leu Leu Ser Val Ala Cys Ser Leu Gly
 20 100 105 110
 Leu Leu Leu Ala Val Ser Leu Thr Val Ala Asn Gly Gly Arg Arg Leu
 115 120 125
 Ile Ala Asp Cys His Pro Gly Leu Leu Asp Pro Leu Val Pro Leu Asp
 130 135 140
 25 Glu Gly Pro Gly His Thr Asp Cys Pro Phe Asp Pro Thr Arg Ile Tyr
 145 150 155 160
 Asp Thr Ala Leu Ala Leu Trp Ile Pro Ser Leu Leu Met Ser Ala Gly
 165 170 175
 Glu Ala Ala Leu Ser Gly Tyr Cys Cys Val Ala Ala Leu Thr Leu Arg
 30 180 185 190
 Gly Val Gly Pro Cys Arg Lys Asp Gly Leu Gln Gly Gln Val Val Ala
 195 200 205

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Gly Cys Asp Ala Arg Val Lys Gln Lys Ala Trp Gln Pro Arg Phe Pro

210

215

220

Gly Ile Lys Val Lys Ala Leu

225

230

5

<210> 6

<211> 97

<212> PRT

<213> Homo sapiens

10

<400> 6

Met Thr Ser Leu Leu Thr Thr Pro Ser Pro Arg Glu Glu Leu Met Thr

1

5

10

15

Thr Pro Ile Leu Gln Pro Thr Glu Ala Leu Ser Pro Glu Asp Gly Ala

15

20

25

30

Ser Thr Ala Leu Ile Ala Val Val Ile Thr Val Val Phe Leu Thr Leu

35

40

45

Leu Ser Val Val Ile Leu Ile Phe Phe Tyr Leu Tyr Lys Asn Lys Gly

50

55

60

20

Ser Tyr Val Thr Tyr Glu Pro Thr Glu Gly Glu Pro Ser Ala Ile Val

65

70

75

80

Gln Met Glu Ser Asp Leu Ala Lys Gly Ser Glu Lys Glu Glu Tyr Phe

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90

95

Ile

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<210> 7

<211> 198

<212> PRT

<213> Homo sapiens

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 20 25 30
 Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile Cys Pro Pro
 5 35 40 45
 Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn Ile Ser Gln Lys
 50 55 60
 Asp Cys Asp Cys Leu His Val Val Glu Pro Met Pro Val Arg Gly Pro
 65 70 75 80
 10 Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu Cys Lys Tyr Glu Glu Arg
 85 90 95
 Ser Ser Val Thr Ile Lys Val Thr Ile Ile Ile Tyr Leu Ser Ile Leu
 100 105 110
 Gly Leu Leu Leu Leu Tyr Met Val Tyr Leu Thr Leu Val Glu Pro Ile
 15 115 120 125
 Leu Lys Arg Arg Leu Phe Gly His Ala Gln Leu Ile Gln Ser Asp Asp
 130 135 140
 Asp Ile Gly Asp His Gln Pro Phe Ala Asn Ala His Asp Val Leu Ala
 145 150 155 160
 20 Arg Ser Arg Ser Arg Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln
 165 170 175
 Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Ser Val Phe Asp
 180 185 190
 Arg His Val Val Leu Ser
 25 195

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 30 <213> Homo sapiens

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 Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp Ser Asn
 20 25 30
 5 Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu Tyr Asp Lys
 35 40 45
 Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr Leu Gly Leu Phe
 50 55 60
 Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val Ser Met Phe Asn Ser
 10 65 70 75 80
 Thr Gln Ser Leu Ile Ser Ile Gly Ala His Cys Ser Ala Ser Val Ala
 85 90 95
 Leu Ser Phe Phe Ile Phe Glu Arg Trp Glu Cys Thr Thr Tyr Trp Tyr
 100 105 110
 15 Ile Phe Val Phe Cys Ser Ala Leu Pro Ala Val Thr Glu Met Ala Leu
 115 120 125
 Phe Val Thr Val Phe Gly Leu Lys Lys Lys Pro Phe
 130 135 140
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 1 5 10 15
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 30 Ala Leu Thr Phe Leu Met Ser Ser Phe Thr Phe Cys Gly Ser Phe Thr
 35 40 45
 Gly Trp Lys Arg His Gly Ala His Ile Tyr Leu Thr Met Leu Leu Ser

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50 55 60

Ile Ala Ile Trp Val Ala Trp Ile Thr Leu Leu Met Leu Pro Asp Phe
65 70 75 80

Asp Arg Arg Trp Asp Asp Thr Ile Leu Ser Ser Ala Leu Ala Ala Asn
5 85 90 95

Gly Trp Val Phe Leu Leu Ala Tyr Val Ser Pro Glu Phe Trp Leu Leu
100 105 110

Thr Lys Gln Arg Asn Pro Met Asp Tyr Pro Val Glu Asp Ala Phe Cys
115 120 125

Lys Pro Gln Leu Val Lys Lys Ser Tyr Gly Val Glu Asn Arg Ala Tyr
10 130 135 140

Ser Gln Glu Glu Ile Thr Gln Gly Phe Glu Glu Thr Gly Asp Thr Leu
145 150 155 160

Tyr Ala Pro Tyr Ser Thr His Phe Gln Leu Gln Asn Gln Pro Pro Gln
15 165 170 175

Lys Glu Phe Ser Ile Pro Arg Ala His Ala Trp Pro Ser Pro Tyr Lys
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Asp Tyr Glu Val Lys Lys Glu Gly Ser
195 200

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<212> PRT
<213> Homo sapiens

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<400> 10

Met Ala Ser Ser Asp Glu Asp Gly Thr Asn Gly Gly Ala Ser Glu Ala
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Gly Glu Asp Arg Glu Ala Pro Gly Lys Arg Arg Arg Leu Gly Phe Leu
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30

Ala Thr Ala Trp Leu Thr Phe Tyr Asp Ile Ala Met Thr Ala Gly Trp
35 40 45

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Leu Val Leu Ala Ile Ala Met Val Arg Phe Tyr Met Glu Lys Gly Thr
 50 55 60
 His Arg Gly Leu Tyr Lys Ser Ile Gln Lys Thr Leu Lys Phe Phe Gln
 65 70 75 80
 5 Thr Phe Ala Leu Leu Glu Ile Val His Cys Leu Ile Gly Ile Val Pro
 85 90 95
 Thr Ser Val Ile Val Thr Gly Val Gln Val Ser Ser Arg Ile Phe Met
 100 105 110
 Val Trp Leu Ile Thr His Ser Ile Lys Pro Ile Gln Asn Glu Glu Ser
 10 115 120 125
 Val Val Leu Phe Leu Val Ala Trp Thr Val Thr Glu Ile Thr Arg Tyr
 130 135 140
 Ser Phe Tyr Thr Phe Ser Leu Leu Asp His Leu Pro Tyr Phe Ile Lys
 145 150 155 160
 15 Trp Ala Arg Tyr Asn Phe Phe Ile Ile Leu Tyr Pro Val Gly Val Ala
 165 170 175
 Gly Glu Leu Leu Thr Ile Tyr Ala Ala Leu Pro His Val Lys Lys Thr
 180 185 190
 Gly Met Phe Ser Ile Arg Leu Pro Asn Lys Tyr Asn Val Ser Phe Asp
 20 195 200 205
 Tyr Tyr Tyr Phe Leu Leu Ile Thr Met Ala Ser Tyr Ile Pro Leu Phe
 210 215 220
 Pro Gln Leu Tyr Phe His Met Leu Arg Gln Arg Arg Lys Val Leu His
 225 230 235 240
 25 Gly Glu Val Ile Val Glu Lys Asp Asp
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<210> 11

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30 <212> DNA

<213> Homo sapiens

FOOESSD"4ES02/60

12/45

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 ttcctgacgt tcattgatct ggttatccag gctgtctttt ttggcatctg tgtgctgact 180
 5 gatctttcca gtcttctgac tcgaggaagt gggaaccagg agcaagagag gcagctcaag 240
 aagctcatct ctctccggga ctggatgcta gctgtgttgg cctttcctgt tggggttttt 300
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 ggcattgtgg tgtacccttt cctggaacac attggcccag gagccagaat catcttcttt 600
 gggctacaa ccatcttaat gaacttctg tacctgctgg gagaagttct gaacaactat 660
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<211> 582

<212> DNA

<213> Homo sapiens

20 <400> 12

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 tccgeggccg ccaggttacg gcagatcac eggtcctttt tctccgccta cctcggetac 180
 cccgggaacc gttcagagct ggtggcgtg atggcggatt ccgtgctctc cgacagcccc 240
 25 ggccccacct ggggcagagt ggtgacgctc gtgaccttcg cagggacgct gctggagaga 300
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 gagggcgacg tcgccggga ctgccagcgc ctggtggcct tgetgagctc ggggtcatg 420
 gggcagcacc gcgcctggct gcaggctcag ggcggctggg atggettttg tcaattcttc 480
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F0050"hes02/60

13/45

<211> 417

<212> DNA

<213> Homo sapiens

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tgtcaaaat	taaacaagt	ggtaattcca	gaattgattg	gccataccat	tgctactgta	180
ttactgetca	tgctattgca	ctggttcctc	ttccttctca	acttacctgt	tgccacttgg	240
aatatatatc	gatacattat	gggtccgagt	ggtaacatgg	gagtgtttga	tccaacagaa	300
atacacaatc	gagggcagct	gaagtcacac	atgaaagaag	ccatgatcaa	gcttggtttc	360
cacttgctct	gcttcttcat	gtatctttat	agtatgatct	tagctttgat	aaatgac	417

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15 <211> 969

<212> DNA

<213> Homo sapiens

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gtcttgggtg	atacggcgctc	ttgccaccgg	gcctgtcagt	tgacctacc	cttgacacacc	180
taccctaagg	aagaggagtt	gtacgcatgt	cagagagggt	gcaggctgtt	ttcaatttgt	240
cagtttgtgg	atgatggaat	tgacttaa	cgaactaa	tggaatgtga	atctgcatgt	300
acagaagcat	attcccaatc	tgatgagcaa	tatgcttgcc	atcttggttg	ccagaatcag	360
ctgccattcg	ctgaactgag	acaagaacaa	cttatgtccc	tgatgccaaa	aatgcaccta	420
ctctttctctc	taactctgggt	gaggtcattc	tggagtgaca	tgatggactc	cgacagagagc	480
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cagtetaagc	cagaaatcca	gtacgcacca	catttgagagc	aggagcctac	aaatttgaga	600
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<212> DNA

<213> Homo sapiens

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 ggcaccgtcc tgcggcacgt ggccaatccc cgcggcgctg tcacgccgga gtacaccgta 180
 15 gccaatgtca tctctgtcgg ctgggggctg ctgagcgctt ccgtgggact tgtggccctc 240
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 gtgaacctgc tcttgctcgt tgccctgctc ctggggcctc ttcttgctgt gtcactcact 360
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 gtaccactgg atgagggggc gggacatact gactgccctt ttgacccac aagaatctat 480
 20 gatacagcct tggtctctct gatcccttct ttgctcatgt ctgcagggga ggctgctcta 540
 tctggttact gctgtgtggc tgcactcact ctacgtggag ttggggccctg caggaaggac 600
 ggacttcagg ggcaggtagt agctgggtgt gacgcaagag tgaaacagaa agcctggcag 660
 ccacggtttc ctgggattaa agtcaaagca tta 693

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<212> DNA

<213> Homo sapiens

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<400> 16

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atcaccggtg tcttctctac cctgctctcg gtcgtgatct tgatcttctt ttacctgtac 180
 aagaacaaag gcagctacgt cacctatgaa cctacagaag gtgagcccag tgccatcgtc 240
 cagatggaga gtgacttggc caagggcagc gagaaagagg aatatttcat c 291

5 <210> 17
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 <212> DNA
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 15 gatgtagaag catactgtct acgctgtgaa tgcaaataatg aagaaagaag ctctgtcaca 300
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 cgctcccgca gtgagccaa cgtgctgaac aaggtagaat atgcacagca gcgctggaag 540
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<210> 18
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 25 <213> Homo sapiens

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 30 ttcacccccg aggagtatga caagcaggac attcagctgg tggccgcgct ctctgtcacc 180
 ctgggcctct ttgcagtga gctggccggc ttctctcag gagtctccat gtccaacagc 240
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atattcgagc gttgggagtg cactacgtat tggtagattt ttgtcttctg cagtgcctt 360
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<210> 19

5 <211> 603

<212> DNA

<213> Homo sapiens

<400> 19

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atgtcctctt ccattgccat ctgggtggcc tggatcaccc tgcctatgt tctgacttt 240
gaccgcaggt gggatgacac cctcctcagc tccgccttgg ctgccaatgg ctgggtgttc 300
15 ctgttggett atgttagtcc cgagttttgg ctgctcaca agcaacgaaa ccccatggat 360
tctcctgttg aggatgcttt ctgtaaacct caactcgtga agaagagcta tgggtgtggag 420
aacagagcct actctcaaga ggaaatcact caaggttttg aagagacagg ggacacgctc 480
tatgccccct attccacaca ttttcagctg cagaaccagc ctccccaaaa ggaattctcc 540
atcccacggg cccacgcttg gccgagcct taaaaagact atgaagtaaa gaaagagggc 600
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<211> 747

<212> DNA

25 <213> Homo sapiens

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30 gacatcgcca tgaccgcggg gtggttggtt ctactattg ccatggtacg tttttatatg 180
gaaaaaggaa cacacagagg tttatataaa agtattcaga agacacttaa atttttccag 240
acatttgctt tgcttgagat agttcactgt ttaattggaa ttgtacctac ttctgtgatt 300

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20	Arg Met Ala Ile Leu Leu Ser Tyr Cys Ser Ile Leu Cys Asn Tyr Lys	
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25	ctg acg ttc att gat ctg gtt atc cag gct gtc ttt ttt ggc atc tgt	196
	Leu Thr Phe Ile Asp Leu Val Ile Gln Ala Val Phe Phe Gly Ile Cys	
	45 50 55	
	gtg ctg act gat ctt tcc agt ctt ctg act cga gga agt ggg aac cag	244
	Val Leu Thr Asp Leu Ser Ser Leu Leu Thr Arg Gly Ser Gly Asn Gln	
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 Asp Asn Phe Ile Pro Gly Trp Leu Asn His Gly Met His Thr Thr Val
 10 125 130 135
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 15 Ser Arg Ser Ser Gly Leu Thr Ala Ile Cys Thr Phe Ser Val Gly Tyr
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 Ile Leu Trp Val Cys Trp Val His His Val Thr Gly Met Trp Val Tyr
 170 175 180 185
 20 cct ttc ctg gaa cac att ggc cca gga gcc aga atc atc ttc ttt ggg 628
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 tct aca acc atc tta atg aac ttc ctg tac ctg ctg gga gaa gtt ctg 676
 Ser Thr Thr Ile Leu Met Asn Phe Leu Tyr Leu Leu Gly Glu Val Leu
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 aac aac tat atc tgg gat aca cag aaa agt atg gaa gaa gag aaa gaa 724
 Asn Asn Tyr Ile Trp Asp Thr Gln Lys Ser Met Glu Glu Glu Lys Glu
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 aagtcattac tgataataac atttttttcc ttttctagtt ttaaaaccag aattggacct 1020
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 30 35 40
 Leu Thr Phe Ile Asp Leu Val Ile Gln Ala Val Phe Phe Gly Ile Cys
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 Val Leu Thr Asp Leu Ser Ser Leu Leu Thr Arg Gly Ser Gly Asn Gln
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 Glu Gln Glu Arg Gln Leu Lys Lys Leu Ile Ser Leu Arg Asp Trp Met
 75 80 85
 25 Leu Ala Val Leu Ala Phe Pro Val Gly Val Phe Val Val Ala Val Phe
 90 95 100 105
 Trp Ile Ile Tyr Ala Tyr Asp Arg Glu Met Ile Tyr Pro Lys Leu Leu
 110 115 120
 Asp Asn Phe Ile Pro Gly Trp Leu Asn His Gly Met His Thr Thr Val
 30 125 130 135
 Leu Pro Phe Ile Leu Ile Glu Met Arg Thr Ser His His Gln Tyr Pro
 140 145 150

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Ser Arg Ser Ser Gly Leu Thr Ala Ile Cys Thr Phe Ser Val Gly Tyr
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 Ile Leu Trp Val Cys Trp Val His His Val Thr Gly Met Trp Val Tyr
 170 175 180 185
 5 Pro Phe Leu Glu His Ile Gly Pro Gly Ala Arg Ile Ile Phe Phe Gly
 190 195 200
 Ser Thr Thr Ile Leu Met Asn Phe Leu Tyr Leu Leu Gly Glu Val Leu
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 Lys Pro Lys Leu Glu
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 Asp Tyr Leu Gly Tyr Cys Ala Arg Glu Pro Gly Thr Pro Glu Pro Ala
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 cca tcc acg ccc gag gcc gcc gtg ctg cgc tcc gcg gcc gcc agg tta 144
 Pro Ser Thr Pro Glu Ala Ala Val Leu Arg Ser Ala Ala Ala Arg Leu
 35 40 45
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5	80					85					90						
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	Gly	Thr	Leu	Leu	Glu	Arg	Gly	Pro	Leu	Val	Thr	Ala	Arg	Trp	Lys	Lys	
	95					100					105					110	
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	Asp	Cys	Gln	Arg	Leu	Val	Ala	Leu	Leu	Ser	Ser	Arg	Leu	Met	Gly	Gln	
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	Phe	Phe	Arg	Thr	Pro	Phe	Pro	Leu	Ala	Phe	Trp	Arg	Lys	Gln	Leu	Val	
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	Gln	Ala	Phe	Leu	Ser	Cys	Leu	Leu	Thr	Thr	Ala	Phe	Ile	Tyr	Leu	Trp	
	175					180					185					190	
	aca	cga	tta	tta	tgagttttaa	aacttttaac	ccgcttctac	ctgcccaact	gt								630
25	Thr	Arg	Leu	Leu													
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	cagacgtttt	tacctgaatg	catacaagga	gtcctgaggt	ggtgatttgg	ccagtgtttt											750
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	taaatgggaa	atacagtgct	atttgctaaa	acttggataa	gagtgcgaac	ctctcatctc											930
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aattctttga aaccaaatcc ttgaaatct aattcctggg acttctaggt ttttatagtt 1110
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35 40 45
Arg Gln Ile His Arg Ser Phe Phe Ser Ala Tyr Leu Gly Tyr Pro Gly
50 55 60
Asn Arg Phe Glu Leu Val Ala Leu Met Ala Asp Ser Val Leu Ser Asp
20 65 70 75
Ser Pro Gly Pro Thr Trp Gly Arg Val Val Thr Leu Val Thr Phe Ala
80 85 90
Gly Thr Leu Leu Glu Arg Gly Pro Leu Val Thr Ala Arg Trp Lys Lys
95 100 105 110
25 Trp Gly Phe Gln Pro Arg Leu Lys Glu Gln Glu Gly Asp Val Ala Arg
115 120 125
Asp Cys Gln Arg Leu Val Ala Leu Leu Ser Ser Arg Leu Met Gly Gln
130 135 140
His Arg Ala Trp Leu Gln Ala Gln Gly Gly Trp Asp Gly Phe Cys His
30 145 150 155
Phe Phe Arg Thr Pro Phe Pro Leu Ala Phe Trp Arg Lys Gln Leu Val
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Gln Ala Phe Leu Ser Cys Leu Leu Thr Thr Ala Phe Ile Tyr Leu Trp
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15 Val Phe Ser Leu Leu Asp Cys Cys Ala Leu Ile Phe Leu Ser Val Tyr

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ttc ata att aca ttg tct gat tta gaa tgt gat tac att aat gct aga 149

Phe Ile Ile Thr Leu Ser Asp Leu Glu Cys Asp Tyr Ile Asn Ala Arg

25

30

35

20 tca tgt tgc tca aaa tta aac aag tgg gta att cca gaa ttg att ggc 197

Ser Cys Cys Ser Lys Leu Asn Lys Trp Val Ile Pro Glu Leu Ile Gly

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45

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cat acc att gtc act gta tta ctg ctc atg tca ttg cac tgg ttc atc 245

His Thr Ile Val Thr Val Leu Leu Leu Met Ser Leu His Trp Phe Ile

25 55 60 65 70

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Phe Leu Leu Asn Leu Pro Val Ala Thr Trp Asn Ile Tyr Arg Tyr Ile

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85

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95

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aat cga ggg cag ctg aag tca cac atg aaa gaa gcc atg atc aag ctt 389

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Gly Phe His Leu Leu Cys Phe Phe Met Tyr Leu Tyr Ser Met Ile Leu
5 120 125 130
gct ttg ata aat gac tgaagctgga gaagccgtgg ttgaagtcag cctacact 490
Ala Leu Ile Asn Asp
135
acagtgcaca gttgaggagc cagagacttc ttaaàatcatc cttagaaccg tgaccatagc 550
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40 45 50
His Thr Ile Val Thr Val Leu Leu Leu Met Ser Leu His Trp Phe Ile
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Phe Leu Leu Asn Leu Pro Val Ala Thr Trp Asn Ile Tyr Arg Tyr Ile
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Thr Ala Ser Cys His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr

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 Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala
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 Glu Leu Arg Gln Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu
 125 130 135 140
 ctc ttt cct cta act ctg gtg agg tca ttc tgg agt gac atg atg gac 484
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 aac tct ggg tgg att tta act aca act ctt gtc ctc tog gtg atg gta 772
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 5 Glu Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg
 285 290 295 300
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 Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala
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 Leu Phe Pro Leu Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp
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 10 Ser Ala Gln Ser Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala
 160 165 170
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 175 180 185
 Ala Pro His Leu Glu Gln Glu Pro Thr Asn Leu Arg Glu Ser Ser Leu
 15 190 195 200
 Ser Lys Met Ser Tyr Leu Gln Met Arg Asn Ser Gln Ala His Arg Asn
 205 210 215 220
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 225 230 235
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 240 245 250
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 255 260 265
 Val Pro Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn
 25 270 275 280
 Glu Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg
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5

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Ala Phe Asp Ala Ala Arg Gly Pro Arg Arg Leu Met Arg Val Gly Leu

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gcg ctg atc ttg gtg ggc cac gtg aac ctg ctg ctg ggg gcc gtg ctg 150

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Ala Leu Ile Leu Val Gly His Val Asn Leu Leu Leu Gly Ala Val Leu

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cat ggc acc gtc ctg cgg cac gtg gcc aat ccc cgc ggc gct gtc acg 198

His Gly Thr Val Leu Arg His Val Ala Asn Pro Arg Gly Ala Val Thr

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95

100

ctc ttg tcc gtt gcc tgc tcc ctg ggc ctc ctt ctt gct gtg tca ctc 390

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Leu Leu Ser Val Ala Cys Ser Leu Gly Leu Leu Leu Ala Val Ser Leu

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110

115

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 Cys Pro Phe Asp Pro Thr Arg Ile Tyr Asp Thr Ala Leu Ala Leu Trp
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 20 220 225 230
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 25 <211> 231
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 <213> Homo sapiens

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10 15 20
 Ala Leu Ile Leu Val Gly His Val Asn Leu Leu Leu Gly Ala Val Leu
 25 30 35
 His Gly Thr Val Leu Arg His Val Ala Asn Pro Arg Gly Ala Val Thr
 5 40 45 50 55
 Pro Glu Tyr Thr Val Ala Asn Val Ile Ser Val Gly Ser Gly Leu Leu
 60 65 70
 Ser Val Ser Val Gly Leu Val Ala Leu Leu Ala Ser Arg Asn Leu Leu
 75 80 85
 10 Arg Pro Pro Leu His Trp Val Leu Leu Ala Leu Ala Leu Val Asn Leu
 90 95 100
 Leu Leu Ser Val Ala Cys Ser Leu Gly Leu Leu Leu Ala Val Ser Leu
 105 110 115
 Thr Val Ala Asn Gly Gly Arg Arg Leu Ile Ala Asp Cys His Pro Gly
 15 120 125 130 135
 Leu Leu Asp Pro Leu Val Pro Leu Asp Glu Gly Pro Gly His Thr Asp
 140 145 150
 Cys Pro Phe Asp Pro Thr Arg Ile Tyr Asp Thr Ala Leu Ala Leu Trp
 155 160 165
 20 Ile Pro Ser Leu Leu Met Ser Ala Gly Glu Ala Ala Leu Ser Gly Tyr
 170 175 180
 Cys Cys Val Ala Ala Leu Thr Leu Arg Gly Val Gly Pro Cys Arg Lys
 185 190 195
 Asp Gly Leu Gln Gly Gln Val Val Ala Gly Cys Asp Ala Arg Val Lys
 25 200 205 210 215
 Gln Lys Ala Trp Gln Pro Arg Phe Pro Gly Ile Lys Val Lys Ala Leu
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<210> 31

30 <211> 1189

<212> DNA

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F0050-1E502260

32/45

<400> 31

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 5 tagctgtgga accctagggc acctgttacc gcgctttggc gaaactgggt tcgctgctga 180
 tttgcgaacc tttgcctgac tttctcaggc cttgagagat ctaagtaaatt ttggtggccc 240
 attgaaagga cctggagaga gctgatgaag atctgcctct tctccaagaa actcaaccac 300
 tagtgaca atg acc agc ctc ctg act act cct tct cca aga gaa gaa ctg 350
 Met Thr Ser Leu Leu Thr Thr Pro Ser Pro Arg Glu Glu Leu
 10 1 5 10
 atg acc acc cca att tta cag ccc act gag gcc ctg tcc cca gaa gat 398
 Met Thr Thr Pro Ile Leu Gln Pro Thr Glu Ala Leu Ser Pro Glu Asp
 15 20 25 30
 gga gcc agc aca gca ctc att gca gtt gtt atc acc gtt gtc ttc ctc 446
 15 Gly Ala Ser Thr Ala Leu Ile Ala Val Val Ile Thr Val Val Phe Leu
 35 40 45
 acc ctg ctc tcg gtc gtg atc ttg atc ttc ttt tac ctg tac aag aac 494
 Thr Leu Leu Ser Val Val Ile Leu Ile Phe Phe Tyr Leu Tyr Lys Asn
 50 55 60
 20 aaa ggc agc tac gtc acc tat gaa cct aca gaa ggt gag ccc agt gcc 542
 Lys Gly Ser Tyr Val Thr Tyr Glu Pro Thr Glu Gly Glu Pro Ser Ala
 65 70 75
 atc gtc cag atg gag agt gac ttg gcc aag ggc agc gag aaa gag gaa 590
 Ile Val Gln Met Glu Ser Asp Leu Ala Lys Gly Ser Glu Lys Glu Glu
 25 80 85 90
 tat ttc atc taatgactcc caggccccaa ggagcttatt cctggetcca t 640
 Tyr Phe Ile
 95
 cgctaacacg ttgactgctt attatgggaa agttttctct gaagccaggg agaagcattg 700
 30 attgatgtgg gcaaattcaa gctccagcca ggtcgcagtc ccaaattgcg acatcactga 760
 ctccagggac cagggacatg gagaaagctg tttatgatat ctttaaccag gccctcttac 820
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33/45

gtgcccagtc atcttttttc acagggtgaa gggagagaaa agattttgag ttaagggtcat 940
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 ccatacaagg tcttcccaga ggctggatac cacagtaaaa ggccaggcca ggaggggtag 1060
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<211> 97

10 <212> PRT

<213> Homo sapiens

<400> 32

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 Met Thr Thr Pro Ile Leu Gln Pro Thr Glu Ala Leu Ser Pro Glu Asp
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 Gly Ala Ser Thr Ala Leu Ile Ala Val Val Ile Thr Val Val Phe Leu
 35 40 45
 20 Thr Leu Leu Ser Val Val Ile Leu Ile Phe Phe Tyr Leu Tyr Lys Asn
 50 55 60
 Lys Gly Ser Tyr Val Thr Tyr Glu Pro Thr Glu Gly Glu Pro Ser Ala
 65 70 75
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 25 80 85 90
 Tyr Phe Ile
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<210> 33

30 <211> 1500

<212> DNA

<213> Homo sapiens

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34/45

<400> 33

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 5 Met Ala Thr Leu Trp Gly Gly
 1 5
 ctt ctt cgg ctt ggc tcc ttg ctc agc ctg tgc tgc ctg gcg ctt tcc 162
 Leu Leu Arg Leu Gly Ser Leu Leu Ser Leu Ser Cys Leu Ala Leu Ser
 10 10 15 20
 gtg ctg ctg ctg gcg cag ctg tca gac gcc gcc aag aat ttc gag gat 210
 Val Leu Leu Leu Ala Gln Leu Ser Asp Ala Ala Lys Asn Phe Glu Asp
 25 30 35
 gtc aga tgt aaa tgt atc tgc cct ccc tat aaa gaa aat tct ggg cat 258
 Val Arg Cys Lys Cys Ile Cys Pro Pro Tyr Lys Glu Asn Ser Gly His
 15 40 45 50 55
 att tat aat aag aac ata tct cag aaa gat tgt gat tgc ctt cat gtt 306
 Ile Tyr Asn Lys Asn Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val
 60 65 70
 gtg gag ccc atg cct gtg cgg ggg cct gat gta gaa gca tac tgt cta 354
 20 Val Glu Pro Met Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu
 75 80 85
 cgc tgt gaa tgc aaa tat gaa gaa aga agc tct gtc aca atc aag gtt 402
 Arg Cys Glu Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val
 90 95 100
 acc att ata att tat ctc tcc att ttg ggc ctt cta ctt ctg tac atg 450
 25 Thr Ile Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Leu Tyr Met
 105 110 115
 gta tat ctt act ctg gtt gag ccc ata ctg aag agg cgc ctc ttt gga 498
 Val Tyr Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly
 30 120 125 130 135
 cat gca cag ttg ata cag agt gat gat gat att ggg gat cac cag cct 546
 His Ala Gln Leu Ile Gln Ser Asp Asp Asp Ile Gly Asp His Gln Pro

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	Phe Ala Asn Ala His Asp Val Leu Ala Arg Ser Arg Ser Arg Ala Asn			
	155	160	165	
5	gtg ctg aac aag gta gaa tat gca cag cag cgc tgg aag ctt caa gtc			642
	Val Leu Asn Lys Val Glu Tyr Ala Gln Gln Arg Trp Lys Leu Gln Val			
	170	175	180	
	caa gag cag cga aag tct gtc ttt gac cgg cat gtt gtc ctc agc			687
	Gln Glu Gln Arg Lys Ser Val Phe Asp Arg His Val Val Leu Ser			
10	185	190	195	
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	agaactgact gggttttgct gggtttcatt ttaatacett gttgatttca ccaactgttg			800
	ctggaagatt caaaactgga agcaaaaact tgcttgattt ttttttcttg ttaacgtaat			860
	aatagagaca tttttaaaag cacacagctc aaagtcagcc aataagtctt ttctatttg			920
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	caagcactct ctttttcacc acatagtttt aacttgactt tcaagataat tttcagggtt			1040
	tttgttgttg ttgttttttg tttgtttggt ttggtgggag aggggagggg tgacctggaa			1100
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Met Ala Thr Leu Trp Gly Gly
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5 Val Leu Leu Leu Ala Gln Leu Ser Asp Ala Ala Lys Asn Phe Glu Asp
 25 30 35

Val Arg Cys Lys Cys Ile Cys Pro Pro Tyr Lys Glu Asn Ser Gly His
 40 45 50 55

Ile Tyr Asn Lys Asn Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val
 10 60 65 70

Val Glu Pro Met Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu
 75 80 85

Arg Cys Glu Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val
 90 95 100

15 Thr Ile Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Leu Tyr Met
 105 110 115

Val Tyr Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly
 120 125 130 135

His Ala Gln Leu Ile Gln Ser Asp Asp Asp Ile Gly Asp His Gln Pro
 20 140 145 150

Phe Ala Asn Ala His Asp Val Leu Ala Arg Ser Arg Ser Arg Ala Asn
 155 160 165

Val Leu Asn Lys Val Glu Tyr Ala Gln Gln Arg Trp Lys Leu Gln Val
 170 175 180

25 Gln Glu Gln Arg Lys Ser Val Phe Asp Arg His Val Val Leu Ser
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<210> 35

<211> 806

30 <212> DNA

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T00E50"4ES02260

37/45

<400> 35

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Met Gly Arg Val Ser Gly Leu

5 1 5
gtg ccc tct cgc ttc ctg acg ctc ctg gcg cat ctg gtg gtc gtc atc 163
Val Pro Ser Arg Phe Leu Thr Leu Leu Ala His Leu Val Val Val Ile

10 10 15 20
acc tta ttc tgg tcc cgg gac agc aac ata cag gcc tgc ctg cct ctc 211
Thr Leu Phe Trp Ser Arg Asp Ser Asn Ile Gln Ala Cys Leu Pro Leu

25 30 35
acg ttc acc ccc gag gag tat gac aag cag gac att cag ctg gtg gcc 259
Thr Phe Thr Pro Glu Glu Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala

40 45 50 55
15 gcg ctc tct gtc acc ctg ggc ctc ttt gca gtg gag ctg gcc ggt ttc 307
Ala Leu Ser Val Thr Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe

60 65 70
ctc tca gga gtc tcc atg ttc aac agc acc cag agc ctc atc tcc att 355
Leu Ser Gly Val Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile

20 75 80 85
ggg gct cac tgt agt gca tcc gtg gcc ctg tcc ttc ttc ata ttc gag 403
Gly Ala His Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu

90 95 100
cgt tgg gag tgc act acg tat tgg tac att ttt gtc ttc tgc agt gcc 451
25 Arg Trp Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala

105 110 115
ctt cca gct gtc act gaa atg gct tta ttc gtc acc gtc ttt ggg ctg 499
Leu Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu

120 125 130 135
30 aaa aag aaa ccc ttc tgattacctt catgacggga acctaaggac gaagcc 550
Lys Lys Lys Pro Phe

38/45

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<212> PRT

10 <213> Homo sapiens

<400> 36

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Thr Leu Phe Trp Ser Arg Asp Ser Asn Ile Gln Ala Cys Leu Pro Leu

25

30

35

Thr Phe Thr Pro Glu Glu Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala

20

40

45

50

55

Ala Leu Ser Val Thr Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe

60

65

70

Leu Ser Gly Val Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile

75

80

85

25 Gly Ala His Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu

90

95

100

Arg Trp Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala

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110

115

Leu Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu

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125

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Lys Lys Lys Pro Phe

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39/45

<210> 37

<211> 1718

<212> DNA

5 <213> Homo sapiens

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	Ala Pro Arg Arg Asn Glu Asp Phe Val Leu Leu Leu Thr Tyr Val Leu	
	15 20 25	
	ttc ttg atg gcg ctg acc ttc ctc atg tcc tcc ttc acc ttc tgt ggt	146
15	Phe Leu Met Ala Leu Thr Phe Leu Met Ser Ser Phe Thr Phe Cys Gly	
	30 35 40 45	
	tcc ttc acg ggc tgg aag aga cat ggg gcc cac atc tac ctc acg atg	194
	Ser Phe Thr Gly Trp Lys Arg His Gly Ala His Ile Tyr Leu Thr Met	
	50 55 60	
20	ctc ctc tcc att gcc atc tgg gtg gcc tgg atc acc ctg ctc atg ctt	242
	Leu Leu Ser Ile Ala Ile Trp Val Ala Trp Ile Thr Leu Leu Met Leu	
	65 70 75	
	cct gac ttt gac cgc agg tgg gat gac acc atc ctc agc tcc gcc ttg	290
	Pro Asp Phe Asp Arg Arg Trp Asp Asp Thr Ile Leu Ser Ser Ala Leu	
25	80 85 90	
	gct gcc aat ggc tgg gtg ttc ctg ttg gct tat gtt agt ccc gag ttt	338
	Ala Ala Asn Gly Trp Val Phe Leu Leu Ala Tyr Val Ser Pro Glu Phe	
	95 100 105	
	tgg ctg ctc aca aag caa cga aac ccc atg gat tat cct gtt gag gat	386
30	Trp Leu Leu Thr Lys Gln Arg Asn Pro Met Asp Tyr Pro Val Glu Asp	
	110 115 120 125	
	gct ttc tgt aaa cct caa ctc gtg aag aag agc tat ggt gtg gag aac	434

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	Ala Phe Cys Lys Pro Gln Leu Val Lys Lys Ser Tyr Gly Val Glu Asn	
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	aga gcc tac tct caa gag gaa atc act caa ggt ttt gaa gag aca ggg	482
	Arg Ala Tyr Ser Gln Glu Glu Ile Thr Gln Gly Phe Glu Glu Thr Gly	
5	145 150 155	
	gac acg ctc tat gcc ccc tat tcc aca cat ttt cag ctg cag aac cag	530
	Asp Thr Leu Tyr Ala Pro Tyr Ser Thr His Phe Gln Leu Gln Asn Gln	
	160 165 170	
	cct ccc caa aag gaa ttc tcc atc cca cgg gcc cac gct tgg ccg agc	578
10	Pro Pro Gln Lys Glu Phe Ser Ile Pro Arg Ala His Ala Trp Pro Ser	
	175 180 185	
	cct tac aaa gac tat gaa gta aag aaa gag ggc agc taactctgtc ctgaag	630
	Pro Tyr Lys Asp Tyr Glu Val Lys Lys Glu Gly Ser	
	190 195 200	
15	agtgggacaa atgcagccgg gcggcagatc tagcgggagc tcaaagggat gtgggcgaaa	690
	tcttgagtct tctgagaaaa ctgtacaaga cactacggga acagtttgcc tccctcccag	750
	cctcaaccac aattcttcca tgctggggct gatgtgggct agtaagactc cagttcttag	810
	aggcgtgtga gtattttttt tttttttgtc tcatccttag gatacttctt ttaagtggga	870
	gtctcaggca actcaagttt agacccttac tctttttgtt tgttttttga aacaggatct	930
20	tgctctgtca cccaggettg agtgcagtgg tgcatcaca gcccagtga gcctcgacca	990
	cctgtgtca agcaatctc ccatctccat ctcccaaagt gctgggatga caggcgtgag	1050
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cactcttt

1718

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<211> 201

5 <212> PRT

<213> Homo sapiens

<400> 38

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 30 35 40 45
 15 Ser Phe Thr Gly Trp Lys Arg His Gly Ala His Ile Tyr Leu Thr Met
 50 55 60
 Leu Leu Ser Ile Ala Ile Trp Val Ala Trp Ile Thr Leu Leu Met Leu
 65 70 75
 Pro Asp Phe Asp Arg Arg Trp Asp Asp Thr Ile Leu Ser Ser Ala Leu
 20 80 85 90
 Ala Ala Asn Gly Trp Val Phe Leu Leu Ala Tyr Val Ser Pro Glu Phe
 95 100 105
 Trp Leu Leu Thr Lys Gln Arg Asn Pro Met Asp Tyr Pro Val Glu Asp
 110 115 120 125
 25 Ala Phe Cys Lys Pro Gln Leu Val Lys Lys Ser Tyr Gly Val Glu Asn
 130 135 140
 Arg Ala Tyr Ser Gln Glu Glu Ile Thr Gln Gly Phe Glu Glu Thr Gly
 145 150 155
 Asp Thr Leu Tyr Ala Pro Tyr Ser Thr His Phe Gln Leu Gln Asn Gln
 30 160 165 170
 Pro Pro Gln Lys Glu Phe Ser Ile Pro Arg Ala His Ala Trp Pro Ser
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Pro Tyr Lys Asp Tyr Glu Val Lys Lys Glu Gly Ser

190

195

200

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<211> 995

<212> DNA

<213> Homo sapiens

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 tgtctccac gtccccaggg tgcgcggcca cc atg gcg tcc agc gac gag gac 173
 Met Ala Ser Ser Asp Glu Asp
 1 5

15 ggc acc aac ggc ggc gcc tcg gag gcc ggc gag gac cgg gag gct ccc 221
 Gly Thr Asn Gly Gly Ala Ser Glu Ala Gly Glu Asp Arg Glu Ala Pro
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ggc aag cgg agg cgc ctg ggg ttc ttg gcc acc gcc tgg ctc acc ttc 269
 Gly Lys Arg Arg Arg Leu Gly Phe Leu Ala Thr Ala Trp Leu Thr Phe

20 25 30 35
 tac gac atc gcc atg acc gcg ggg tgg ttg gtt cta gct att gcc atg 317
 Tyr Asp Ile Ala Met Thr Ala Gly Trp Leu Val Leu Ala Ile Ala Met
 40 45 50 55

gta cgt ttt tat atg gaa aaa gga aca cac aga ggt tta tat aaa agt 365
 25 Val Arg Phe Tyr Met Glu Lys Gly Thr His Arg Gly Leu Tyr Lys Ser
 60 65 70

att cag aag aca ctt aaa ttt ttc cag aca ttt gcc ttg ctt gag ata 413
 Ile Gln Lys Thr Leu Lys Phe Phe Gln Thr Phe Ala Leu Leu Glu Ile
 75 80 85

30 gtt cac tgt tta att gga att gta cct act tct gtg att gtg act ggg 461
 Val His Cys Leu Ile Gly Ile Val Pro Thr Ser Val Ile Val Thr Gly
 90 95 100

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 Val Gln Val Ser Ser Arg Ile Phe Met Val Trp Leu Ile Thr His Ser
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 ata aaa cca atc cag aat gaa gag agt gtg gtg ctt ttt ctg gtc gcg 557
 5 Ile Lys Pro Ile Gln Asn Glu Glu Ser Val Val Leu Phe Leu Val Ala
 120 125 130 135
 tgg act gtg aca gag atc act cgc tat tcc ttc tac aca ttc agc ctt 605
 Trp Thr Val Thr Glu Ile Thr Arg Tyr Ser Phe Tyr Thr Phe Ser Leu
 140 145 150
 10 ctt gac cac ttg cca tac ttc att aaa tgg gcc aga tat aat ttt ttt 653
 Leu Asp His Leu Pro Tyr Phe Ile Lys Trp Ala Arg Tyr Asn Phe Phe
 155 160 165
 atc atc tta tat cct gtt gga gtt gct ggt gaa ctt ctt aca ata tac 701
 Ile Ile Leu Tyr Pro Val Gly Val Ala Gly Glu Leu Leu Thr Ile Tyr
 15 170 175 180
 gct gcc ttg ccg cat gtg aag aaa aca gga atg ttt tca ata aga ctt 749
 Ala Ala Leu Pro His Val Lys Lys Thr Gly Met Phe Ser Ile Arg Leu
 185 190 195
 cct aac aaa tac aat gtc tct ttt gac tac tat tat ttt ctt ctt ata 797
 20 Pro Asn Lys Tyr Asn Val Ser Phe Asp Tyr Tyr Tyr Phe Leu Leu Ile
 200 205 210 215
 acc atg gca tca tat ata cct ttg ttt cca caa ctc tat ttt cat atg 845
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 220 225 230
 25 tta cgt caa aga aga aag gtg ctt cat gga gag gtg att gta gaa aag 893
 Leu Arg Gln Arg Arg Lys Val Leu His Gly Glu Val Ile Val Glu Lys
 235 240 245
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 30 gagtccaagt ttttaataaca agaataaaca actttgtgaa atatc 995

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<210> 40

<211> 249

<212> PRT

<213> Homo sapiens

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<400> 40

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 25 30 35
 Tyr Asp Ile Ala Met Thr Ala Gly Trp Leu Val Leu Ala Ile Ala Met
 40 45 50 55
 15 Val Arg Phe Tyr Met Glu Lys Gly Thr His Arg Gly Leu Tyr Lys Ser
 60 65 70
 Ile Gln Lys Thr Leu Lys Phe Phe Gln Thr Phe Ala Leu Leu Glu Ile
 75 80 85
 Val His Cys Leu Ile Gly Ile Val Pro Thr Ser Val Ile Val Thr Gly
 20 90 95 100
 Val Gln Val Ser Ser Arg Ile Phe Met Val Trp Leu Ile Thr His Ser
 105 110 115
 Ile Lys Pro Ile Gln Asn Glu Glu Ser Val Val Leu Phe Leu Val Ala
 120 125 130 135
 25 Trp Thr Val Thr Glu Ile Thr Arg Tyr Ser Phe Tyr Thr Phe Ser Leu
 140 145 150
 Leu Asp His Leu Pro Tyr Phe Ile Lys Trp Ala Arg Tyr Asn Phe Phe
 155 160 165
 Ile Ile Leu Tyr Pro Val Gly Val Ala Gly Glu Leu Leu Thr Ile Tyr
 30 170 175 180
 Ala Ala Leu Pro His Val Lys Lys Thr Gly Met Phe Ser Ile Arg Leu
 185 190 195

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45/45

Pro Asn Lys Tyr Asn Val Ser Phe Asp Tyr Tyr Tyr Phe Leu Leu Ile
200 205 210 215
Thr Met Ala Ser Tyr Ile Pro Leu Phe Pro Gln Leu Tyr Phe His Met
220 225 230
5 Leu Arg Gln Arg Arg Lys Val Leu His Gly Glu Val Ile Val Glu Lys
235 240 245
Asp Asp

TUESDAY, FEBRUARY 2, 2000